

09/847586

CORPORATE SOURCE: Natl. Inst. Neurol. Commun. Disorders Stroke,
Natl. Inst. Health, Bethesda, MD, 20892, USA
SOURCE: EMBO Journal (1988), 7(7), 1947-55
CODEN: EMJODG; ISSN: 0261-4189

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Genomic clones for the largest human neurofilament protein (NF-H) were isolated, the intron/exon boundaries mapped, and the entire protein-coding regions (exons) sequenced. The predicted protein contains a central region that obeys the structural criteria identified for α -helical 'rod' domains typically present in all intermediate filament (IF) protein components; it is .apprx.310 amino acids long, shares amino acid sequence homol. with other IF protein rod domains, and displays the characteristic heptad repeats of apolar amino acids which facilitate coiled-coil interaction. Nevertheless, anomalies are noted in the structure of the F-H rod which could explain observations of its poor homopolymeric assembly in vitro. The protein segment on the carboxy-terminal side of the human NF-H rod is uniquely long (>600 amino acids) compared to other IF proteins and is highly charged (>24% Glu, >25% Lys), rich in proline (>12%), and impoverished in cysteine, methionine, and aromatic amino acids. Its most remarkable feature is repetitive sequence that covers more than half its length and includes the sequence motif, Lys-Ser-Pro (KSP), >40 times. Together with the identification of the serine in KSP as the main target for NF-directed protein kinases in vivo, this repetitive character explains the massive phosphorylation of the NF-H subunit that can occur in axons. The human NF-H gene has three introns, two of which interrupt the protein-coding sequence at identical points to introns in the genes for the two smaller NF proteins, NF-M and NF-L. Both these introns differ from any of the several introns that have a common organization in all other (non-neural) IF genes. However, a clear evolutionary relationship between neural and non-neural IFs is now revealed by the observation that the third intron in the NF-H gene matches the position of one of the conserved introns in the non-neural IF gene pattern. Hence, divergence of the two IF lineages (neural from non-neural) is more likely to have involved ancestral IF gene duplication rather than RNA-mediated transposition.

IT 119213-37-5, Phosphoprotein NF-H (human clone HW10/HW12 subunit protein moiety reduced)

RL: PRP (Properties)
(amino acid sequence of)

E27 THROUGH E53 ASSIGNED

FILE 'REGISTRY' ENTERED AT 11:49:29 ON 26 MAY 2004

L3 27 SEA FILE=REGISTRY ABB=ON PLU=ON (391971-89-4/BI OR
119213-37-5/BI OR 147388-28-1/BI OR 222963-40-8/BI OR
329019-83-2/BI OR 329020-41-9/BI OR 329020-42-0/BI OR
329020-43-1/BI OR 329020-44-2/BI OR 329020-45-3/BI OR
329020-46-4/BI OR 329020-47-5/BI OR 329020-48-6/BI OR
355029-63-9/BI OR 355043-60-6/BI OR 374653-90-4/BI OR
400113-81-7/BI OR 400154-00-9/BI OR 409392-10-5/BI OR
419604-01-6/BI OR 420909-41-7/BI OR 437023-11-5/BI OR
528612-99-9/BI OR 538425-66-0/BI OR 538458-06-9/BI OR

Searcher : Shears 571-272-2528

09/847586

611252-43-8/BI OR 612112-12-6/BI)

L4 27 L1 AND L3

L4 ANSWER 1 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 612112-12-6 REGISTRY

CN Protein (human heart clone GenBank gi:10835089 mitochondria-associated) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1115: PN: W003087768 SEQID: 1115 claimed protein

CI MAN

SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLLHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEA E AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTS LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQLDAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLEEGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKS EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEAAA SPEKEAKSPV KEEAKSPAEA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA KEAKSPA EAKSPA
601 PEKAKSPVKE EAKSPA EAKS EVKSPEKAKS PTKEEAKSPE
651 KAKSPEKAKS PEKEEAKSPE KAKSPVKA EA KSPEKAKSPV KAEAKSPEKA
=
701 KSPVKEEAKS PEKAKSPVKE EAKSPEKAKS PVKEEAKTPE KAKSPVKEEA
===== =
751 KSPEKAKSPE KAKTLDVKSP EAKTPAKEEA RSPADKFPEK AKSPVKEEVK
=====
801 SPEKAKSPLK EDAKAPEKEI PKKEEVKSPV KEEKPKQEVK VKEPPKAAEE
851 EKAPATPKTE EKKDSKKEEA PKKEAPKPKV EEKKEPAVEK PKESKVEAKK
901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPKE KTEVAKKEPD DAKAKEPSKP
951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTL SK EPSKPKAEKA
1001 EKSSSTDQKD SKPPEKATED KAAKGK

HITS AT: 700-731, 742-759

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:333132

L4 ANSWER 2 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 611252-43-8 REGISTRY

CN Protein (human clone US20030194704-SEQID-32114 exon-derived fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 114: PN: US20030194704 SEQID: 32114 claimed protein

CI MAN

SQL 617

SEQ 1 KLEEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPA EAKSP EKEEAKSPA E VKSPEKAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPA EKEAK SPAEAKSPEK

09/847586

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201 AKSPVKEEAK SPAEAKSPVK EEAKSPA EVK SPEKAKSPTK EEAKSPEKAK
251 SPEKEEAKSP EKAKSPVKA E AKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
=====
301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
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351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPKEKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
601 DSKPPEKATE DKAAGK
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HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:303033

L4 ANSWER 3 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 538458-06-9 REGISTRY
CN Pain-regulated protein (human clone W003016475-SEQID-9347) (9CI)
(CA INDEX NAME)
OTHER NAMES:
CN 2255: PN: W003016475 SEQID: 9347 claimed protein
CI MAN
SQL 1020

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SEQ 1 MMSFGGADAL LGAPFAPLHG GGS LHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDV TSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQLDAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLLGE E CRIGFGPIPF SLPEGLPKIP SVSTHIKVK E EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEEA SPEKEAKSPV KEEAKSPA EA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA KE EAKSPA EAKS
601 PEKAKSPVKE EAKSPA EAKS PVKEEAKSPA EVKSPEKAKS PTKEEAKSPE
651 KAKSPEKEEA KSPEKAKSPV KAEAKSPEKA KSPVKA EAKS PEKAKSPVKE
=====
701 EAKSPEKAKS PVKEEAKSPE KAKSPVKEEA KTPEKAKSPV KEEAKSPEKA
=====
751 KSPEKAKTLD VKSPEAKTPA KEEARSPADK FPEKAKSPVK EEVKSPEKAK
=====
801 SPLKADAKAP EKEIPKKEEV KSPVKEEEKP QEVKVKEPPK KAEE EKAPAT
851 PKTEEEKDSK KEEAPKKEAP KPKVEEKKEP AVEKPKESKV EAKKEEAEDK
901 KKVPTPEKEA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
951 APEKKDTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKA EKSSST
1001 DQKDSKPPEK ATEDKAAGK
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HITS AT: 694-725, 736-753

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:18399

09/847586

L4 ANSWER 4 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 538425-66-0 REGISTRY
CN Pain-regulated protein (human clone WO03016475-SEQID-4798) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 2214: PN: WO03016475 SEQID: 4798 claimed protein
CI MAN
SQL 1020

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSILHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTS LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQDLAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLEEGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKs EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA EAKSPA EAKS
601 PEKAKSPVKE EAKSPA EAKS PVKEEAKSPA EVKSPEKAKS PTKEEAKSPE
651 KAKSPEKEEA KSPEKAKSPV KAEAKSPEKA KSPVKAEAKS PEKAKSPVKE
=====

701 EAKSPEKAKS PVKEEAKSPE KAKSPVKEEA KTPEKAKSPV KEEAKSPEKA
=====

751 KSPEKAKTLD VKSPEAKTPA KEEARSPADK FPEKAKSPVK EEVKSPEKAK
=====

801 SPLKADAKAP EKEIPKKEEV KSPVKEEEKP QEVKVKEPPK KAEEEKAPAT
851 PKTEEEKKDSK KEEAPKKEAP KPKVEEKKEP AVEKPKESKV EAKKEEAEDK
901 KKVPTPEKEA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
951 APEKDKTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKAEKSSST
1001 DQKDSKPPEK ATEDKAAKKG

HITS AT: 694-725, 736-753

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:18398

L4 ANSWER 5 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 528612-99-9 REGISTRY
CN Protein (human gene CG4399 sequence homolog) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 130: PN: WO03040301 PAGE: 197-198 claimed protein
CN Putative neurofilament protein (human)
CI MAN
SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSILHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTS LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQDLAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA

09/847586

401 AYRKLEEGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVK EEEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPA EA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA KE EAKSPA EAKS
601 PEKAKSPVKE EAKSPA EAKS PVKEEAKSPA EVKSPEKAKS PTKEEAKSPE
651 KAKSPEKAKS PEKEEAKSPE KAKSPVKA EA KSPEKAKSPV KAEAKSPEKA
=
701 KSPVKEEAKS PEKAKSPVKE EAKSPEKAKS PVKEEAKTPE KAKSPVKEEA
===== =
751 KSPEKAKSPE KAKTLDVKSP EAKTPAKEEA RSPADKFPEK AKSPVKEEVK
=====
801 SPEKAKSPLK EDAKAPEKEI PKKEEVKSPV KEEEEKPQEVK VKEPPKKAEE
851 EKAPATPKTE EKKDSKKEEA PKKEAPKPKV EEKKEPAVEK PKESKVEAKK
901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPKE KTEVAKKEPD DAKAKEPSK
951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTLSK EPSKPKAEKA
1001 EKSSSTDQKD SKPPEKATED KAAKGK

HITS AT: 700-731, 742-759

REFERENCE 1: 138:397302

L4 ANSWER 6 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 437023-11-5 REGISTRY
CN Protein (human clone US20020048763-SEQID-36182 exon-encoded
fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1177: PN: US20020048763 SEQID: 36182 claimed protein

CI MAN

SQL 617

SEQ 1 KLEEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEEK IKVVEKSEKE
51 TVIVVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPA EAKSP EKEEAKSPA E VKSPEKAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPA EKEAK SPAEAKSPEK
201 AKSPVKEEAK SPAEAKSPVK EEAKSPA EVK SPEKAKSPTK EEAKSPEKAK
251 SPEKEEAKSP EKAKSPVKA E AKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
=====
301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
===== =
351 EAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKKA E EKAPATPKT
451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
601 DSKPPEKATE DKAAGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:28982

L4 ANSWER 7 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 420909-41-7 REGISTRY
CN Protein (human clone WO01057273-SEQID-28953 exon-encoded fragment)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2760: PN: WO01057273 SEQID: 28953 claimed protein

Searcher : Shears 571-272-2528

09/847586

CI MAN
SQL 617

SEQ 1 KLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPAE VKSPEKAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAKEEAK SPAEAKSPEK
201 AKSPVKEEAK SPAEAKSPVK EEAKSPA EVK SPEKAKSPTK EEAKSPEKAK
251 SPEKEEAKSP EKAKSPVKA E AKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
=====

301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
===== == =====

351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPKEKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
601 DSKPPEKATE DKAAGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351355

L4 ANSWER 8 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 419604-01-6 REGISTRY
CN Protein (human cervix cell clone WO0157278-SEQID-21284 exon-encoded
fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1884: PN: WO0157278 SEQID: 21284 claimed protein
CI MAN
SQL 617

SEQ 1 KLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPAE VKSPEKAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAKEEAK SPAEAKSPEK
201 AKSPVKEEAK SPAEAKSPVK EEAKSPA EVK SPEKAKSPTK EEAKSPEKAK
251 SPEKEEAKSP EKAKSPVKA E AKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
=====

301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
===== == =====

351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPKEKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
601 DSKPPEKATE DKAAGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351347

L4 ANSWER 9 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 409392-10-5 REGISTRY

09/847586

CN Protein (human brain clone W00157275-SEQID-28374 exon-encoded
fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2394: PN: W00157275 SEQID: 28374 claimed protein

CI MAN

SQL 617

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SEQ      1 KLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
      51 TVIVVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
     101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPAE VKSPEKAKSP
     151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAKEEAK SPAEAKSPEK
     201 AKSPVKEEAK SPAEAKSPVK EEAKSPAENVK SPEKAKSPTK EEAKSPEKAK
     251 SPEKEEAKSP EKAKSPVKA EAKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
           =====
     301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
           =====
     351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
     401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
     451 EEKDKSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
     501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
     551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
     601 DSKPPEKATE DKAAGK
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HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:305084

L4 ANSWER 10 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 400154-00-9 REGISTRY

CN Protein (human fetal liver clone W00157277-SEQID-28080 exon-encoded
fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2295: PN: W00157277 SEQID: 28080 claimed protein

CI MAN

SQL 617

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SEQ      1 KLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
      51 TVIVVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
     101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPAE VKSPEKAKSP
     151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAKEEAK SPAEAKSPEK
     201 AKSPVKEEAK SPAEAKSPVK EEAKSPAENVK SPEKAKSPTK EEAKSPEKAK
     251 SPEKEEAKSP EKAKSPVKA EAKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
           =====
     301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
           =====
     351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
     401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
     451 EEKDKSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
     501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
     551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
     601 DSKPPEKATE DKAAGK
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HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

09/847586

REFERENCE 1: 136:178933

L4 ANSWER 11 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 400113-81-7 REGISTRY
CN Protein (human clone W00157274-SEQID-22654 exon-encoded fragment)
(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2061: PN: W00157274 SEQID: 22654 claimed protein
CI MAN
SQL 617

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SEQ      1 KLLGEEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
      51 TVVIEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
     101 PPAEEAASPE KEAKSPVKEE AKSPAIAKSP EKEEAKSPAE VKSPEKAKSP
     151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEAK SPAEAKSPEK
     201 AKSPVKEEAK SPAEAKSPVK EEAKSPAIVK SPEKAKSPTK EEAKSPEKAK
     251 SPEKEEAKSP EKAKSPVKA EAKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
           =====
     301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EAKSPVKEE AKSPEKAKSP
           =====
     351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
     401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
     451 EEKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
     501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
     551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAE AEKSSSTDQK
     601 DSKPPEKATE DKAAGK
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HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:195264

L4 ANSWER 12 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 391971-89-4 REGISTRY
CN Heavy neurofilament subunit (human gene NF-H) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4211: PN: W003038130 FIGURE: 3 claimed protein
CN GenBank CAA33366
CN GenBank CAA33366 (Translated from: GenBank X15306)
CI MAN
SQL 1020

```
SEQ      1 MMSFGGADAL LGAPFAPLHG GGSLLHYALAR KGGAGGTRSA AGSSSGFHSW
      51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
     101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
     151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
     201 ALARFAQAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
     251 AQAQMQAETR DALKCDVTS LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
     301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
     351 DRHQADIASY QEAIQQLDAE LRNTKWEMAA QLREYQDLN VKMALDIEIA
     401 AYRKLLGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVS EEKIKVVEKS
     451 EKETVIVIEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEGGE EEEAEGGEEEE
     501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAIA KSPEKEEAKS PAEVKSPEKA
     551 KSPAEEAKS PPEAKSPEKE EAKSPAIVKS PEKAKSPAIA EAKSPAIAKS
     601 PEKAKSPVKE EAKSPAIAKS PVKEEAKSPA EVKSPEKAKS PTKEEAKSPE
     651 KAKSPEKEEA KSPEKAKSPV KAEAKSPEKA KSPVKAIAKS PEKAKSPVKE
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09/847586

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=====
701 EAKSPEKAKS PVKEEAKSPE KAKSPVKEEA KTPEKAKSPV KEEAKSPEKA
=====
751 KSPEKAKTLD VKSPEAKTPA KEEARSPADK FPEKAKSPVK EEVKSPEKAK
=====
801 SPLKADAKAP EKEIPKKEEV KSPVKEEEKP QEVKVKEPPK KAEEEKAPAT
851 PKTEEEKKDSK KEEAPKKEAP KPKVEEKKEP AVEKPKESKV EAKKEEAEDK
901 KKVPTPEKEA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
951 APEKKDTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKAEKSSST
1001 DQKDSKPPEK ATEDKAAKKG
HITS AT: 694-725, 736-753
```

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:380506

REFERENCE 2: 136:146104

L4 ANSWER 13 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 374653-90-4 REGISTRY

CN Protein (human HBL100 cell clone W00157270-SEQID-12927 exon-encoded fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2869: PN: W00157270 SEQID: 12927 claimed protein

CI MAN

SQL 617

```
SEQ      1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
      51 TVIVVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEE AEGGEEETKS
     101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPAE VKSPEKAKSP
     151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAKEEAK SPAEAKSPEK
     201 AKSPVKEEAK SPAEAKSPVK EEAKSPAEVK SPEKAKSPTK EEAKSPEKAK
     251 SPEKEEAKSP EKAKSPVKA EAKSPEKAKSP VKAEAKSPEK AKSPVKEEAK
=====
    301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EKAKSPVKEE AKSPEKAKSP
=====
    351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEKAKSPL
    401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKKA EEEKAPATPKT
    451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
    501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
    551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSKPKAEK AEKSSSTDQK
    601 DSKPPEKATE DKAAGK
```

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:1595

L4 ANSWER 14 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 355043-60-6 REGISTRY

CN Protein (human clone 787CIP2B_152 contig-encoded fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 338: PN: W00157190 SEQID: 3455 claimed sequence

CI MAN

SQL 1033

Searcher : Shears 571-272-2528

09/847586

SEQ 1 APTAQAMMSF GGADALLGAP FAPLHGGGSL HYALARKGGA GGTRSAAGSS
51 SGFHSWTRTS VSSVSASPSR FRGAGAASST DSLDTLSNGP EGCMAVAVATS
101 RSEKEQLQAL NDRFAGYIDK VRQLEAHNRS LEGEAAALRQ QQAGRSAMGE
151 LYEREVREMR GAVLRLGAAR GQLRLEQEH LEDIAHVQR LDDEARQREE
201 AEAARALAR FAQEAEAARV DLQKKAQALQ EECGYLRRHH QEEVGELLGQ
251 IQGSGAAQAA MQAETRDALK CDVTSALREI RAQLEGHAVQ STLQSEWFR
301 VRLDRLSEAA KVNTDAMRSA QEEITEYRRQ LQARTTELEA LKSTKDSLER
351 QRSELEDHRQ ADIASYQEAI QQLDAELRNT KWEMAAQLRE YQDLLNVKMA
401 LDIEIAAYRK LLEGEERIG FGPIPFSLPE GLPKIPSVST HIKVKSEEKI
451 KVVEKSEKET VIVEEQTEET QVTEEVTEEE DKEAKEEEGK EEEGEEEEEA
501 EGGEETKSP PAEEAASPEK EAKSPVKEEA KSPAEAKSPE KEEAKSPA EV
551 KSPEKAKSPA KEEAKSPPEA KSPEKDGKQ FQAEVKSPEK AKSPAKEEAK
601 SPAEAKSPEK AKSPVKEEAK SPAEAKSPVK EEAKSPA EVK SPEKAKSPTK
651 EEAKSPEKAK SPEKAKSPEK EEAKSPEKAK SPVKA EAKSPV KAE
701 AKSPEKAKSP VKEEAKSPEK AKSPVKEEAK SPEKAKSPVK EEAKTPEKAK
===== ==
751 SPVKEEAKSP EAKSPEKAK TLDVKSPEAK TPAKEEARSP ADKFPEKAKS
===== ==
801 PVKEEVKSPE KAKSPLKEDA KAPEKEIPKK EEVKS PVKEE EKPQEVKVKE
851 PPKAAEEKA PATPKTEEEK DSKKEEAPKK EAPKPKVEEK KEPAVEKPKE
901 SKVEAKKEEA EDKKKVPTPE KEAPAKVEVK EDAKPKEKTE VAKKEPDDAK
951 AKEPSKPAEK KEAAPEKKDT KEEKAKKPEE KPKTEAKAKE DDKTLSKEPS
1001 KPKA EKA EKS SSTQKDSKP PEKATEDKAA KGK

HITS AT: 707-738, 749-766

REFERENCE 1: 135:176460

L4 ANSWER 15 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 355029-63-9 REGISTRY

CN Protein (human clone 787CIP2B_152) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 795: PN: WO0157190 SEQID: 1487 claimed protein

CI MAN

SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGS LHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDEAR QREEAEAAAR
201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTS LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQLDAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLLEGE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKs EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEEGEEEGGE EEEAEGGEEE
501 TKSPPVVEEA SPEKEAKSPV KEEAKSPA EA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA KE EAKSPA EAKS
601 PEKAKSPVKE EAKSPA EAKS PVKEEAKSPA EVKSPEKAKS PTKEEAKSPE
651 KAKSPEKAKS PEKEEAKSPE KAKSPVKA EA KSPEKAKSPV KAEAKSPEKA
=
701 KSPVKEEAKS PEKAKSPVKE EAKSPEKAKS PVKEEAKTPE KAKSPVKEEA
===== ==
751 KSPEKAKSPE KAKTLDVKS P EA KTPAKEEA RSPADKFPEK AKSPVKEEVK
===== ==
801 SPEKAKSPLK EDAKAPEKEI PKKEEVKSPV KEEKPKQEVK VKEPPKAE

Searcher : Shears 571-272-2528

09/847586

851 EKAPATPKTE EKKDSKKEEA PKKEAPKPKV EEKKEPAVEK PKESKVEAKK
901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPKE KTEVAKKEPD DAKAKEPSKP
951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTLSK EPSKPKAEKA
1001 EKSSSTDQKD SKPPEKATED KAAKGK
HITS AT: 700-731, 742-759

REFERENCE 1: 135:176460

L4 . ANSWER 16 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-48-6 REGISTRY
CN L-Valinamide, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-
L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-
phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-
lysyl-O-phosphono-L-seryl-L-prolyl- (9CI) (CA INDEX NAME)
SQL 19

SEQ 1 AKSPVKEEAK SPEKAKSPV
=====
HITS AT: 1-18

REFERENCE 1: 134:204745

L4 ANSWER 17 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-47-5 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-
lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-
phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-
lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====
HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 18 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-46-4 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L-
 α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-
seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-
phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====
HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 19 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-45-3 REGISTRY

Searcher : Shears 571-272-2528

09/847586

CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)

SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP

=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 20 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 329020-44-2 REGISTRY

CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)

SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP

=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 21 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 329020-43-1 REGISTRY

CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)

SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP

=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 22 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 329020-42-0 REGISTRY

CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)

SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP

=====

Searcher : Shears 571-272-2528

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 23 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 329020-41-9 REGISTRY
 CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI)
 (CA INDEX NAME)
 SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
 =====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 24 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 329019-83-2 REGISTRY
 CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI)
 (CA INDEX NAME)
 SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
 =====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 25 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 222963-40-8 REGISTRY
 CN Protein (human brain gene KIAA0845 C-terminal fragment) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank BAA74868
 CN GenBank BAA74868 (Translated from: GenBank AB020652)
 CI MAN
 SQL 1034

SEQ 1 NPISTAQAMM SFGGADALLG APFAPLHGGG SLHYALARKG GAGGTRSAAG
 51 SSSGFHSWTR TSVSSVSASP SRFRGAGAAS STDSLDTLSN GPEGCMVAVA
 101 TSRSEKEQLQ ALNDRFAGYI DKVRQLEAHN RSLEGEAAAL RQQQAGRSAM
 151 GELYEREVRE MRGAVLRLGA ARGQLRLEQE HLLEDIAHVR QRLDDEARQR
 201 EEAEAAARAL ARFAQEAEAA RVDLQKKAQA LQEECGYLRR HHQEEVGELL
 251 GQIQGSGAAQ AQMQAETRDA LKCDVTSALR EIRAQLEGHA VQSTLQSEEW
 301 FRVRLDRLSE AAKVNTDAMR SAQEEITEYR RQLQARTTEL EALKSTKDSL
 351 ERQRSELEDR HQADIASYQE AIQQLDAELR NTKWEMAAQL REYQDLLNVK

09/847586

401 MALDIEIAAY RKLLEGEECR IGFGPIPFSL PEGLPKIPSV STHIKVKSEE
451 KIKVVEKSEK ETVIVVEEQTE ETQVTEEVTE EEEKEAKEEE GKEEEGEEEE
501 EAEGGEEETK SPPAEEAASP EKEAKSPVKE EAKSPAEEAKS PEKEEAKSPA
551 EVKSPEKA KS KAKSPVKEEA KSPAEAKSPV KEEAKSPA EV KSPEKAKSPT
601 KSPAEAKSPE KAKSPVKEEA KSPAEAKSPV KEEAKSPA EV KSPEKAKSPT
651 KEEAKSPEKA KSPEKAKSPE KEEAKSPEKA KSPVKAEEAKS PEKAKSPVKA
701 EAKSPEKA KS PVKEEAKSPE KAKSPVKEEA KSPEKAKSPV KEEAKTPEKA
=====
751 KSPVKEEAKS PEKAKSPEKA KTLDVKSPEA KTPAKEEARS PADKFPEKAK
=====
801 SPVKEEVKSP EAKSPLKED AKAPEKEIPK KEEVKSPVKE EEKPQEVKVK
851 EPPKKAEEEEK APATPKTEEK KDSKKEEAPK KEAPKPKVEE KKEPAVEKPK
901 ESKVEAKKEE AEDKKKVPTP EKEAPAKVEV KEDAKPKTEKT EVAKKEPDDA
951 KAKEPSKPAE KKEAAPEKED TKEEKAKKPE EKPKTEAKAK EDDKTLKSKP
1001 SKPKAEKAEK SSSTDQKDSK PPEKATEDKA AKGK
HITS AT: 708-739, 750-767

REFERENCE 1: 130:292252

L4 ANSWER 26 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 147388-28-1 REGISTRY
CN Phosphoprotein NF-H (rabbit isoform 1 C-terminal fragment) (9CI)
(CA INDEX NAME)
CI MAN
SQL 606

SEQ 1 EKETVIVEEQ TEEIQVTEEV TEEEEEKEAKE EEGGEEEEAK SPTEGGAASP
51 EEEAKSPA EA KSPVKEEAKS PAEAKSPA EA KSPA EAKSPE KAKSPVKEEA
=====
101 KSPEKAKSPV KEEAKSPA EA KSPEKAKSPA EAKSPEKA KS PVKEEAKSPE
=====
151 KAKSPA EAKS PEKAKSPA EA KSPEKAKSPV KEEAKSPEKA KSPVKEEAKS
=====
201 PAEAKSPEKA KSPVKEEAKS PEKAKSPA EA KSPVKEEAKS PEKAKSPEKE
=====
251 EAKSPA EAKS PEKAKSPEKA KSPVEVKSPA EAKSPEKA KS PVKEEAKSPE
=====
301 KAKSPVKEEA KSPEKAKSPV KEEAKSPEKA KSPVKEEAKS PEKAKSPVKE
=====
351 EAKSPEKA KS PVKEEAKSPE KAKSPEKA KS PVKEEAKSPE KAKSPVKEEA
=====
401 KSPEKAKSPV KEEAKSPEKE TPKKEEVKVK EPPKKVEETA PAPPKVEKDS
=====
451 KKDEAPKKEA PKPAVEKPK STAEAKKDEA EDKKKAAPAK MEGKEEAKPK
501 EKTEVAKKEP EDAKAKEPSK PTEKEPEKPK KEETPAAPVK KEAKEEARKP
551 EEKPKTEAKA KEDDKALSKE PSKPKTEKAE KSSSTDQKDS RPPEKATEDK
601 AAKGEK
HITS AT: 92-109, 138-155, 176-193, 210-227, 230-247, 288-375,
378-409

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 118:206731

L4 ANSWER 27 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 119213-37-5 REGISTRY

Searcher : Shears 571-272-2528

09/847586

CN Phosphoprotein NF-H (human clone HW10/HW12 subunit protein moiety
reduced) (9CI) (CA INDEX NAME)

CI MAN

SQL 1054

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLLHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQDLAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLLGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKs EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKS PEKAKSPA KEAKSPPEAKS
601 PEKEEAKSPA EVKSPEKAKS PAKEEAKSPA EAKSPEKAKS PVKEEAKSPA
651 EAKSPVKEEA KSPA EVKSPE KAKSPTKEEA KSPEKAKSPE KEEAKSPEKA
701 KSPVKA EAKS PEKAKSPVKA EAKSPEKAKS PVKEEAKSPE KAKSPVKEEA
=====

751 KSPEKAKSPV KEEAKTPEKA KSPVKEEAKS PEKAKSPEKA KTLDVKSPEA
=====

801 KTPAKEEARS PADKFPEKAK SPVKEEVKSP EKAKSPLKAD AKAPEKEIPK
851 KEEVKSPVKE EEKPEVKVK EPPKKA EEEK APATPKTEEK KDSKKEEAPK
901 KEAPKPKVEE KKEPAVEKPK ESKVEAKKEE AEDKKKVPTP EKEAPAKVEV
951 KEDAKPKEKT EVAKKEPDDA KAKEPSKPAE KKEAAPEKPD TKEEKAKKPE
1001 EKPKEAKAK EDDKTLSEK SKPKAEKAEK SSSTDQKDSK PPEKATEDKA
1051 AKGK

HITS AT: 728-759, 770-787

REFERENCE 1: 110:89623

=> fil hom

FILE 'HOME' ENTERED AT 11:49:53 ON 26 MAY 2004